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| APPLICATION NO. | FILING DATE | FIRST NAMED INVENTOR | ATTORNEY DOCKET NO. | CONFIRMATION NO. |
|---|---|---|---|---|
| 09/771,503 | 01/26/2001 | Henry Yue | PC-0027 US | 6227 |

27904 7590 03/12/2003

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| EXAMINER |
|---|
| CANELLA, KAREN A |

| ART UNIT | PAPER NUMBER |
|---|---|
| 1642 | |

DATE MAILED: 03/12/2003

15

Please find below and/or attached an Office communication concerning this application or proceeding.

# Office Action Summary

| Application No. | Applicant(s) |
|---|---|
| 09/771,503 | Yue et al |
| **Examiner** | **Art Unit** |
| Karen Canella | 1642 |

*-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --*

**Period for Reply**

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *3 months* MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136 (a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

**Status**

1) ☐ Responsive to communication(s) filed on _____.

2a) ☐ This action is FINAL. 2b) ☒ This action is non-final.

3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11; 453 O.G. 213.

**Disposition of Claims**

4) ☒ Claim(s) *1-21* is/are pending in the application.

4a) Of the above, claim(s) *14-21* is/are withdrawn from consideration.

5) ☒ Claim(s) *3* is/are allowed.

6) ☒ Claim(s) *1, 2, and 4-13* is/are rejected.

7) ☐ Claim(s) _____ is/are objected to.

8) ☐ Claims _____ are subject to restriction and/or election requirement.

**Application Papers**

9) ☒ The specification is objected to by the Examiner.

10) ☐ The drawing(s) filed on _____ is/are a) ☐ accepted or b) ☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11) ☐ The proposed drawing correction filed on _____ is: a) ☐ approved b) ☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12) ☒ The oath or declaration is objected to by the Examiner.

**Priority under 35 U.S.C. §§ 119 and 120**

13) ☐ Acknowledgement is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a) ☐ All b) ☐ Some* c) ☐ None of:

1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. _____.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

*See the attached detailed Office action for a list of the certified copies not received.

14) ☐ Acknowledgement is made of a claim for domestic priority under 35 U.S.C. § 119(e).

a) ☐ The translation of the foreign language provisional application has been received.

15) ☐ Acknowledgement is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

**Attachment(s)**

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s). _____
4) ☐ Interview Summary (PTO-413) Paper No(s). _____
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: attachment

***Response to Amendment***

1. Claims 14-21 remain withdrawn from consideration. Claims 1-13 are under consideration.

2. After review and reconsideration, the finality of the Office action of Paper No. 12 is withdrawn.

3. The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office Action.

***Claim Rejections Withdrawn***

4. The rejected of claims 1-13 under 35 U.S.C. 101 because the claimed invention is not supported by either a specific, substantial asserted utility or a well-established utility is withdrawn in light of applicants arguments.

5. The rejection of claims 1-13 under 35 U.S.C. 112, first paragraph, for lacking enablement due to the lack of a specific, substantial or well-established utility is withdrawn in light of applicants arguments.

***New Grounds of Rejection***

6. The disclosure is objected for failing to state the relationship between the instant application and PCT/US99/22685 in the first line of the specification. Amendment of the specification to state that the instant application is a continuation or a continuation in part of said PCT is required.

7. The oath or declaration is defective. A new oath or declaration in compliance with 37 CFR 1.67(a) identifying this application by application number and filing date is required. See MPEP §§ 602.01 and 602.02.

The oath or declaration is defective because:

It fails to claim benefit to PCT/US99/2265 and U.S. provisional application 60/240,943. In the event that the instant application is a CIP of the PCT the Oath/Declaration should state that the person making the oath or declaration in a continuation-in-part application filed under the conditions specified in 35 U.S.C. 120 which discloses and claims subject matter in addition to that disclosed in the prior copending application, acknowledges the duty to disclose to the Office all information known to the person to be material to patentability as defined in 37 CFR 1.56 which occurred between the filing date of the prior application and the national or PCT international filing date of the continuation-in-part application.

8. The specification is objected to as failing to provide proper antecedent basis for the claimed subject matter. See 37 CFR 1.75(d)(1) and MPEP § 608.01(o). Correction of the following is required: Page 11, line 20 indicates that SEQ ID NO:3 and the variant SEQ ID NO:7 both products of claim 2, share sequence homology over residues 381 to 971. However, SEQ ID NO:3 consists of 276 residues in total and the sequence homology indicates an 82% identity over 591 residues. In the event that SEQ ID NO:3 were completely homologous across 276 residues of a 591 residue segment of SEQ ID NO:7 that would result in a sequence homology of 46.7%.

9. Claim 6 is rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter. Amendment of the claim to recite an isolated host cell would obviate this rejection.

10.The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

11. Claims 1-7, 11 and 13 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 1 recites and isolated cDNA comprising a nucleic acid sequence...or a complement thereof. It is unclear if complement thereof refers to the nucleic acid sequence or the isolated cDNA. Dependent claims 4-13 are rendered vague and indefinite as it is unclear if they are limited to cDNA encoding the protein of claim 1, or if they embody the complement of said cDNA. For purpose of examination, the claims will be read as encompassing both cDNA encoding a protein, and a complement thereof.

Claim 2a recites "a fragment of SEQ ID NO:2 selected from SEQ ID NO:3-5 or the complement thereof. It is unclear if complements thereof refers to SEQ ID NO:3-5 or fragments of SEQ ID NO:2.

Claim 7 recites a method comprising the culturing of a host cell of claim 6 under conditions for protein expression and recovering the protein from the host cell culture. However, it is unclear that the protein encoded by the cDNA of claim 1 is recovered from culture. Host cells express many proteins which are endogenous to the cell itself in addition to proteins encoded by the expression vector which are expressed by the cDNA of claim 2, such as beta-lactamase, or other proteins involved in selective antibiotic resistance or selective growth. Without a limitation such as the statement that the recovered protein is the protein encoded by SEQ ID NO:2, it is unclear what protein is being produced.

Claim 11 is drawn to a method for using a cDNA to detect expression of a nucleic acid in a sample comprising hybridizing the composition of claim 4 to a nucleic acid sample under conditions to form at least one hybridization complex; and detecting hybridization complex formation, wherein complex formation indicates expression of the nucleic acid in the sample, wherein the cDNA is differentially expressed when compared with a standard and diagnostic of colon cancer or colon polyps. The method is vague and indefinite in that there is no definition or limitation for "a standard"; and there is no active method step linking the outcome of comparison with said standard to the diagnosis of colon cancer or colon polyps.

Claim 13 recites an improper Markush Group. Applicant is referred to the M.P.E.P. section 2173.05(h) and advised to amend the claim to read ---peptides or transcription factor---in order to obviate this rejection.

12. Claims 2 and 7-13 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. .

(A)As drawn to polynucleotides comprising EST sequences

Claim 2 is drawn to an isolated DNA comprising SEQ ID NO:3-5 or the complement of SEQ ID NO:3-5. SEQ ID NO:3-5 are partial DNA sequences consisting of residues 1-276, 1-497 and 1-606 of SEQ ID NO:2. Claim 2 is drawn to a genus of nucleic acids in that it encompasses any nucleic acid sequence that minimal comprises SEQ ID NO:3- within it, including any full gene which contains the sequence, and any fusion constructs. The specification does not address whether the partial cDNA sequences cross exon/intron splice junctions which would exclude the possibility of the claims reading on a full length gene. Therefore when given the broadest reasonable interpretation the claim encompasses full length genes and cDNAs that are not fully described. It is noted that the description of a full length open reading frame is not a description of a gene as eukaryotic genes are expected to have introns and regulatory regions, such as promoters.

A description of a genus of nucleic acids may be achieved by means of recitation of representative number of cDNAs defined by nucleotide sequence falling within the scope of the genus which features constitute a substantial portion of the genus. Regents of the University of California v. Eli Lily & Co, 119 F3d 1559, 1569, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997).

Here the specification discloses only SEQ ID NO:3-5 as structural features shared by members of the claimed genus. Since the claimed genus encompasses genes yet to be discovered,

and DNA construct that encode fusion proteins, the structural features of SEQ ID NO:3-5 do not constitute a substantial portion of the claimed genus. Therefore, the disclosure of SEQ ID NO:3-5 does not provide an adequate description of the claimed genus. Amendment of product claims drawn to SEQ ID NO:3-5 to nucleic acids consiting of, rather then comprising, would obviate this part of the rejection.

(B)As drawn to a method for using a CDNA to produce a protein, wherein said cDNA is the complementary sequence to SEQ ID NO:2, and as drawn to methods of using a cDNA to detect expression of a nucleic acid, wherein said cDNA is not the complementary sequence to SEQ ID NO:2.

Claim 8 is drawn to a method for using a cDNA to detect expression of a nucleic acid in a sample comprising hybridizing the composition of claim 4 to nucleic acid in the sample. Claim 4 clearly encompasses both the cDNA of claim 1 and the complement of the isolated nucleic acid of claim 1. Thus, claim 8 is drawn in part to a method of using the nucleic acid encoding SEQ ID NO:1 for the detection of expression of nucleic acids within a sample. Claim 7 is drawn to a method of using a cDNA to produce a protein wherein either the cDNA encoding SEQ NO:1 or the complement of said cDNA is used to produce a protein. Claims 7-11 depend upon a genus of expressed nucleic acids encompassing nucleic acids which encode intelectin and nucleic acids which encode a completely unrelated protein, as nucleic acids which hybridize to SEQ ID NO:2 would translate in the reverse of SEQ ID NO:2 and therefore would not encode intelectin or be expected to encode any protein related to intelectin. The specification teaches a method of using the complementary nucleic acid to the nucleic acids which encode SEQ ID NO:1 for the detection of the nucleic acids encoding intelectin within a sample. Since the claims depend upon a protein yet to be discovered, i.e. the translated product of the sequence which hybridizes to the nucleic acids encoding SEQ ID NO:1, the disclosure of SEQ ID NO:2 is insufficient to describe the claimed genus.

(C)As drawn to a method of using a cDNA to screen a plurality of molecules which specifically bind the cDNA (peptides, transcription factors).

Claim 12 is drawn to a method for using a cDNA to screen a plurality of molecules or compounds the method comprising combining the cDNA of claim 1 with a plurality of molecules under conditions to allow for specific binding, detecting the specific binding, thereby identifying a molecule of compound which specifically binds to the cDNA. Claims 13 embodies the molecules or compounds of DNA, RNA, peptide nuclei acids, artificial chromosomes, peptides or transcription factors. The claims rely on a genus of molecules and compounds which specifically bind to the cDNA of claim 1. There are no structural or functional restrictions on the plurality of molecules or compounds used in the method. The specification has disclosed complementary nucleic acid sequences which will specifically binds to the expressed nucleic acid sequence of SEQ ID NO:1, or to the nucleic acids which encode the amino acid sequence of SEQ ID NO:1. Thus, the disclosure adequately describes the genus of nucleic acids molecules encompassing RNA, DNA, peptide nucleic acid and artificial chromosome constructs. However, the genus of molecules and compounds also includes peptides and transcription factors. The specification has not disclosed a peptide, protein or transcription factor which would bind to the disclosed cDNA. Thus the disclosure of nucleic acids as molecules which will bind to the claimed cDNA doe not anticipate the structural or functional features of peptides and transcription factors, therefore the disclosure of he nucleic acids which encode SEQ ID NO:1, SEQ ID NO:2-5 or complements of aforesaid nucleic acid sequences does not provide an adequate description of genus of molecules and compounds relied upon in the methods of claims 12 and 13.

13. Claims 4 and 8-11 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for detecting the expressed nucleic acid of SEQ ID NO:2 or the nucleic acids encoding SEQ ID NO:1, does not reasonably provide enablement for the detection of the nucleic acids comprising the complement of SEQ ID NO:2 or the complement of

the nucleic acids encoding SEQ ID NO:1. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims. Claim 8 is drawn to a method for using a cDNA to detect expression of a nucleic acid in a sample comprising hybridizing the composition of claim 4 to nucleic acid in said sample. Claim 4 clearly encompasses both the cDNA of claim 1 and the complement of the isolated nucleic acid of claim 1. Thus, claim 8 is drawn in part to a method of using the nucleic acid encoding SEQ ID NO:1 for the detection of expression of nucleic acids within a sample. For the reasons stated above, sequence which are complementary to SEQ ID NO:2 or the nucleic acids encoding SEQ ID NO:1 would not be expected to encode intelectin or a protein similar to intelectin. It is not known how one of skill in the art would use the detection of the hybridization complex between the composition of claim 4 comprising the cDNA sequence of claim 1 and a labeling moiety and the expressed nucleic acids in a sample, as said hybridization complex would not be expected to be indicative of colon cancer or polyps. One of skill in the art would be subject to undue experimentation without reasonable expectation of success in order practice the broadly claimed invention.

14. Claims 1, 2, 4-10, 12 and 13 are rejected under 35 U.S.C. 102(e) as being anticipated by Pierce et al (U.S. 6,146,849). Claims 1 is drawn in part to the complement of an isolated cDNA comprising a nucleic acid sequence encoding SEQ ID NO:1. Claim 2 is drawn in part to the complement of: an isolated DNA sequence comprising SEQ ID NO:2; SEQ ID NO:3, 4 and 5. Claim 4 embodies the complement of claim 1 and a labeling moiety. Claim 5 is drawn to a vector comprising the cDNA of claim 1. Claim 6 is drawn to a host cell comprising the vector of claim 5. Claim 7 is drawn to a method of producing a protein comprising culturing the host cell of claim 6,. Claim 8 is drawn to a method for using a cDNA to detect expression of a nucleic acid comprising hybridizing the composition of claim 4 to nucleic acid in a sample and detecting the hybridization complex. Claim 9 is drawn to the method of claim 8 further comprising amplifying

the nucleic acid in the sample prior to hybridization. Claim 10 embodies the method of claim 8 wherein the composition is attached to a substrate. Claim 12 is drawn to a method of using a cDNA to screen a plurality of molecules or compounds under conditions to allow specific binding, and detecting specific binding, thereby identifying a molecule or compound which specifically binds to the cDNA. Claims 13 specifically embodies the method of claim 12 wherein the molecules or compounds are selected from DNA, RNA, peptide nuclei acids, artificial chromosomes constructions, peptides or transcription factors.

It is noted that the metes and bounds of claim 1 cannot be determined as it is unclear if the "complement thereof" is part of the isolated cDNA. When given the broadest reasonable interpretation, the claim is read as encompassing this alternative. The specification defines "complement" on page 7, lines 11-13, as a nucleic acid sequence which will hybridize to cDNA or mRNA under conditions of high stringency. Pierce et al disclose the cDNA clone of HL-13 (SEQ ID NO:5) which encodes (nucleotides 34-1011, column 3, lines 56-61) an amino acid sequence identical to the instant SEQ ID NO:1 with the exception of an arginine residue at position 103. The complement of this CDNA would hybridize under stringent conditions to the instant SEQ ID NO:2 because there is only one nucleotide difference out of 975 nucleotides of coding region, as the substitution of a "A" for the "G" as nucleotide position 341 of the attached sequence alignment would result in the substitution of His for Arg. Furthermore, the instant SEQ ID NO:3-5 would hybridize to the complement of the coding sequence of SEQ ID NO:5 as there would be no mismatched nucleotides for SEQ ID NO:3, and only a single mismatched nucleotide for SEQ ID NO:4 and 5. Pierce et al disclose that at conditions of high stringency, molecules having about 95-100% sequence identity form hybridization complexes (column 4, lines 14-20) which would encompass the instant SEQ ID NO:2-5 and the cDNA encoding the instant SEQ ID NO:1. Pierce et al disclose the pQE-9 QIAexpress vector comprising HL-13, and the expression of said vector in E coli to obtain the recombinant protein (column 10, lines 15-35 and column 17, lines 43-51), this fulfilling the specific embodiments of claims 5-7. Pierce et al disclose a method for

detecting the expression of a HL-13 nucleic acid in a sample comprising the use of radio labeled probes. (Column 13, lines 1-19, Table 3 and column 18, lines 9-35), thus fulfilling the specific embodiments of claim 8.. Pierce et al teach detection of hybridization complexes with expressed DNA by means of Northern Blot analysis, therefore the radio labeled probes would be attached to the membrane after washing, thus fulfilling the specific embodiment of claim 10. The probes used by Pierce et al comprise complementary sequence which would hybridize under stringent conditions to the nucleic acid encoding SEQ ID NO:1. Pierce et al disclose that the expression of the HL-13 nucleic acid was detected in the human small intestine stretch lambda gt10 cDNA library (column 25, lines 23-29). The mRNA used to make the library was subjected to amplification by a reverse polymerase in the synthesis of cDNA from RNA, thus fulfilling the limitation of claim 9 drawn to amplification of the nucleic acids prior to hybridization. Further, Pierce et al disclose that somatic cell hybrid DNAs were screened by PCR prior to FISH analysis, again fulfilling the specific embodiment of claims 8 and 9 (column 27, lines 16-50). Pierce et al disclose primers used to make genomic clones comprising nucleic acids which would hybridize under stringent conditions to the nucleic acid which encode SEQ ID NO:1, thus fulfilling the specific embodiment of claims 12 and claim 13, drawn to artificial chromosome constructs.

Pierce et al disclose a method of using a cDNA to screen a plurality of molecules or compounds comprising the hybridization of radio labeled probes that would hybridize under stringent conditions to the nucleic acid sequence encoding SEQ ID NO:1 to the lambda stretch gt10 cDNA library (column 25, lines 23-29), and in Norther blots with various tissues (column 18, lines 9-35), thus fulfilling the limitations of claims 12 and 13, drawn to DNA molecules and RNA molecules.

15. Claims 1 and 2 are rejected under 35 U.S.C. 102(b) as being anticipated by The New England Biolabs Catalog (1993-1994, page 91). The New England Biolabs Catalog discloses

random hexamers which will be complementary across their full length to the nucleic acids encoding SEQ ID NO:1 and SEQ ID NO:2-5.

***Conclusion***

16. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Karen Canella whose telephone number is (703) 308-8362. The examiner can normally be reached on Monday through Friday from 8:30 am to 6:00 pm. A message may be left on the examiner's voice mail service. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anthony Caputa, can be reached on (703) 308-3995. Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Karen A. Canella, Ph.D.
Patent Examiner, Group 1642
March 1, 2003

ANTHONY C. CAPUTA
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

attachment

US-09-124-758-5

alignment_scores:
Quality: 208.00 Length: 309
Ratio: 0.675 Gaps: 0
Percent Similarity: 99.676 Percent Identity: 99.676

alignment_block:
US-09-771-503-1 x US-09-124-758-5

Align seg 1/1 to: US-09-124-758-5 from: 1 to: 1139

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      1 MetLeuSerMetLeuArgThrMetThrArgLeuCysPheLeuLeuPhePh 17
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     34 ATGCTGTCCATGCTGAGGACAATGACCAGACTCTGCTTCCTGTTATTCTT 83

     17 eSerValAlaThrSerGlyCysSerAlaAlaAlaAlaSerSerLeuGluM 34
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     84 CTCTGTGGCCACCAGTGGGTGCAGTGCAGCAGCAGCCTCTTCTCTTGAGA 133

     34 etLeuSerArgGluPheGluThrCysAlaPheSerPheSerSerLeuPro 50
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    134 TGCTCTCGAGGGAATTCGAAACCTGTGCCTTCTCCTTTTCTTCCCTGCCT 183

     51 ArgSerCysLysGluIleLysGluArgCysHisSerAlaGlyAspGlyLe 67
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    184 AGAAGCTGCAAAGAAATCAAGGAACGCTGCCATAGTGCAGGTGATGGCCT 233

     67 uTyrPheLeuArgThrLysAsnGlyValValTyrGlnThrPheCysAspM 84
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    234 GTATTTTCTCCGCACCAAGAATGGTGTTGTCTACCAGACCTTCTGTGACA 283

     84 etThrSerGlyGlyGlyGlyTrpThrLeuValAlaSerValHisGluAsn 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    284 TGACTTCTGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCACGAGAAT 333

    101 AspMetHisGlyLysCysThrValGlyAspArgTrpSerSerGlnGlnGl 117
        ||||||  ||||||||||||||||||||||||||||||||||||||||||
    334 GACATGCGTGGGAAGTGCACGGTGGGTGATCGCTGGTCCAGTCAGCAGGG 383

    117 yAsnLysAlaAspTyrProGluGlyAspGlyAsnTrpAlaAsnTyrAsnT 134
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    384 CAACAAAGCAGACTACCCAGAGGGGGATGGCAACTGGGCCAACTACAACA 433

    134 hrPheGlySerAlaGluAlaAlaThrSerAspAspTyrLysAsnProGly 150
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    434 CCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCTGGC 483

    151 TyrTyrAspIleGlnAlaLysAspLeuGlyIleTrpHisValProAsnLy 167
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    484 TACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCATGTGCCCAACAA 533

    167 sSerProMetGlnHisTrpArgAsnSerAlaLeuLeuArgTyrArgThrA 184
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    534 GTCCCCCATGCAGCATTGGAGAAACAGCGCCCTGCTGAGGTACCGCACCA 583

    184 snThrGlyPheLeuGlnArgLeuGlyHisAsnLeuPheGlyIleTyrGln 200
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    584 ACACTGGCTTCCTCCAGAGACTGGGACATAATCTGTTTGGCATCTACCAG 633

    201 LysTyrProValLysTyrArgSerGlyLysCysTrpAsnAspAsnGlyPr 217
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    634 AAATACCCAGTGAAATACAGATCAGGGAAATGTTGGAATGACAATGGCCC 683

    217 oAlaIleProValValTyrAspPheGlyAspAlaLysLysThrAlaSerT 234
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    684 AGCCATACCTGTGGTCTATGACTTTGGTGATGCTAAGAAGACTGCATCTT 733

    234 yrTyrSerProTyrGlyGlnArgGluPheValAlaGlyPheValGlnPhe 250
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    734 ATTACTCACCGTATGGTCAACGGGAATTTGTTGCAGGATTCGTTCAGTTC 783

    251 ArgValPheAsnAsnGluArgAlaAlaAsnAlaLeuCysAlaGlyIleLy 267
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    784 CGGGTGTTTAATAACGAGAGAGCAGCCAACGCCCTTTGTGCTGGGATAAA 833

    267 sValThrGlyCysAsnThrGluHisHisCysIleGlyGlyGlyGlyPheP 284
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    834 AGTTACTGGCTGTAACACTGAGCATCACTGCATCGGTGGAGGAGGGTTCT 883

    284 heProGlnGlyLysProArgGlnCysGlyAspPheSerAlaPheAspTrp 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    884 TCCCACAGGGCAAACCCCGTCAGTGTGGGGACTTCTCCGCCTTTGACTGG 933

    301 AspGlyTyrGlyThrHisValLysSer 309
        |||||||||||||||||||||||||
    934 GATGGATATGGAACTCACGTTAAGAGC 960
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